

REMARKS

The present application was filed on February 20, 2004 with claims 1-19. Claims 4-7, 10-12, 15, 16, 18 and 19 have been withdrawn.

In the outstanding Office Action dated June 13, 2007, the Examiner: (i) rejected claims 13 and 14 under 35 U.S.C. §101; (ii) rejected claims 1-3, 8, 9, 13, 14 and 17 under 35 U.S.C. §112, second paragraph; and (iii) rejected claims 1-3, 8, 9, 13, 14 and 17 under 35 U.S.C. §102(b) as being anticipated by U.S. Patent No. 5,706,498 to Fujimiya et al. (hereinafter “Fujimiya”).

With regard to the §101 rejection of claims 13 and 14, such claims have been amended to more clearly recite statutory subject matter. More specifically, the claims have been amended to recite a method for making a computer implemented process to enable the screening of nucleotide sequences by instantiating a series of computer instructions onto a computer readable medium. Accordingly, withdrawal of the rejection of claims 13 and 14 under 35 U.S.C. §101 is therefore respectfully requested.

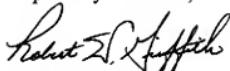
With regard to the rejection of claims 1-3, 8, 9, 13, 14 and 17 under 35 U.S.C. §112, second paragraph, the claims have been amended to more clearly point out and distinctly claim the subject matter which the applicant regards as the invention. Accordingly, withdrawal of the rejection of claims 1-3, 8, 9, 13, 14 and 17 under 35 U.S.C. §112 is therefore respectfully requested.

With regard to the rejection of claims 1-3, 8, 9, 13, 14 and 17 under 35 U.S.C. §102(b) as being anticipated by Fujimiya, Applicant asserts that Fujimiya fails to teach or suggest each and every element of the claims as amended. Fujimiya discloses a gene database retrieval system that retrieves a gene sequence having a sequence similar to a sequence similar to sequence data from a gene database. Further Fujimiya discloses a determination of a degree of similarity between target data and key data. However, Fujimiya fails to disclose the evaluation of a binding possibility of target nucleotide sequence data to complementary sequence data via a determination of whether the complementary sequence data is similar to a subsequence of the target nucleotide sequence data in descending order of edit distance of binding precision, wherein the edit distance is the number of times nucleotide characters of the subsequence are required to be adjusted to generate the

complementary sequence data, as recited in independent claims 1, 8, 13 and 17. Further, Fujimiya fails to disclose the storing of a maximum acceptable edit distance of binding precision between a target nucleotide sequence and a probe nucleotide sequence, as recited in independent claims 8, 13 and 17. Support for this amendment can be found on page 13, lines 9-27, and page 15, line 10 through page 16, line 11 of the Specification. Dependent claims 2, 3, 9 and 14 are patentable at least by virtue of their dependency from independent claims 1, 8 and 13 and also recite patentable subject matter in their own right. Accordingly, withdrawal of the rejection of claims 1-3, 8, 9, 13, 14 and 17 under 35 U.S.C. §102(b) is therefore respectfully requested.

In view of the above, Applicant believes that claims 1-19 are in condition for allowance, and respectfully request withdrawal of the §101, §112 and §102(b) rejections.

Respectfully submitted,



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